

CERTIFICATE OF EXPRESS MAIL

NUMBER EL611000538

DATE OF DEPOSIT April 24, 2001

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:

Yu

Group Art Unit: Unknown

Serial No.: Unknown

Examiner: Unknown

Filed: Concurrently Herewith

Atty. Dkt. No.: INDA:002USC1

For: MU OPIOID RECEPTOR METHODS (as amended)

REQUEST FOR TRANSFER OF SEQUENCE LISTING UNDER 37 C.F.R. § 1.821(e)

BOX SEQUENCE

Commissioner for Patents
Washington, D.C. 20231

Commissioner:

Pursuant to 37 C.F.R. § 1.821(e), Applicant respectfully requests that the sequence information previously submitted in parent application ("parent application"), U.S. Serial No. 08/120,601 filed September 13, 1993, be transferred to and used in the above-referenced patent application ("instant application"). Only one computer readable sequence listing was submitted to the U.S. Patent and Trademark Office in the parent application. The sequence information in the instant application is identical to the sequence information contained in the previously-filed computer readable sequence listing in the parent application. It is understood that the U.S. Patent and Trademark Office will make the necessary change in application number and filing date of

the computer readable form that will be used for the instant application. A paper copy of the sequence listing is included in the originally-filed specification of the instant application.

Applicant requests the transfer of the previously-filed computer readable sequence listing from the parent application to the instant application is in lieu of filing a duplicate computer readable sequence listing.

No fee is believed to be due in connection with the filing of this document; however, should any fees under 37 C.F.R. §§ 1.16 to 1.21 be deemed necessary for any reason relating to this document, the Commissioner is hereby authorized to deduct said fee from Fulbright & Jaworski Account No.: 50-1212/10010779/GNS.

Respectfully submitted,



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Date: April 24, 2001

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Yu, Lei
- (ii) TITLE OF INVENTION: Mu Opioid Receptors:
Compositions and Methods
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Arnold, White & Durkee
 - (B) STREET: 321 North Clark Street, Suite 800
 - (C) CITY: Chicago
 - (D) STATE: IL
 - (E) COUNTRY: USA
 - (F) ZIP: 60610
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Northrup, Thomas E.
 - (B) REGISTRATION NUMBER: 33,268
 - (C) REFERENCE/DOCKET NUMBER: ARCD095
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 312-744-0090
 - (B) TELEFAX: 312-755-4489

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1618 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (cdna)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 214..1410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGTGGAAGGG GGCTACAAGC AGAGGAGAAT ATCAGACGCT CAGACGTTCC CTTCTGCCTG	60
CCGCTCTTCT CTGGTTCCAC TAGGGCTGGT CCATGTAAGA ATCTGACGGA GCCTAGGGCA	120
GCTGTGAGAG GAAGAGGCTG GGGCGCGTGG AACCCGAAAA GTCTGAGTGC TCTCAGTTAC	180
AGCCTACCTA GTCCGCAGCA GGCCTTCAGC ACC ATG GAC AGC AGC ACC GGC CCA	234
Met Asp Ser Ser Thr Gly Pro	
5	

Sub
B1

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cont*

GGG AAC ACC AGC GAC TGC TCA GAC CCC TTA GCT CAG GCA AGT TGC TCC	282
Gly Asn Thr Ser Asp Cys Ser Asp Pro Leu Ala Gln Ala Ser Cys Ser	
10 15 20	
CCA GCA CCT GGC TCC TGG CTC AAC TTG TCC CAC GTT GAT GGC AAC CAG	330
Pro Ala Pro Gly Ser Trp Leu Asn Leu Ser His Val Asp Gly Asn Gln	
25 30 35	
TCC GAT CCA TGC GGT CTG AAC CGC ACC GGG CTT GGC GGC AAC GAC AGC	378
Ser Asp Pro Cys Gly Leu Asn Arg Thr Gly Leu Gly Gly Asn Asp Ser	
40 45 50 55	
CTG TGC CCT CAG ACC GGC AGC CCT TCC ATG GTC ACA GCC ATT ACC ATC	426
Leu Cys Pro Gln Thr Gly Ser Pro Ser Met Val Thr Ala Ile Thr Ile	
60 65 70	
ATG GCC CTC TAC TCT ATC GTG TGT GTA GTG GGC CTC TTC GGA AAC TTC	474
Met Ala Leu Tyr Ser Ile Val Cys Val Val Gly Leu Phe Gly Asn Phe	
75 80 85	
CTG GTC ATG TAT GTG ATT GTA AGA TAC ACC AAA ATG AAG ACT GCC ACC	522
Leu Val Met Tyr Val Ile Val Arg Tyr Thr Lys Met Lys Thr Ala Thr	
90 95 100	
AAC ATC TAC ATT TTC AAC CTT GCT CTG GCA GAC GCC TTA GCG ACC AGT	570
Asn Ile Tyr Ile Phe Asn Leu Ala Leu Ala Asp Ala Leu Ala Thr Ser	
105 110 115	
ACA CTG CCC TTT CAG AGT GTC AAC TAC CTG ATG GGA ACA TGG CCC TTC	618
Thr Leu Pro Phe Gln Ser Val Asn Tyr Leu Met Gly Thr Trp Pro Phe	
120 125 130 135	
GGA ACC ATC CTC TGC AAG ATC GTG ATC TCA ATA GAT TAC TAC AAC ATG	666
Gly Thr Ile Leu Cys Lys Ile Val Ile Ser Ile Asp Tyr Tyr Asn Met	
140 145 150	
TTC ACC AGC ATA TTC ACC CTC TGC ACC ATG AGC GTG GAC CGC TAC ATT	714
Phe Thr Ser Ile Phe Thr Leu Cys Thr Met Ser Val Asp Arg Tyr Ile	
155 160 165	
GCT GTC TGC CAC CCA GTC AAA GCC CTG GAT TTC CGT ACC CCC CGA AAT	762
Ala Val Cys His Pro Val Lys Ala Leu Asp Phe Arg Thr Pro Arg Asn	
170 175 180	
GCC AAA ATC GTC AAC GTC TGC AAC TGG ATC CTC TCT TCT GCC ATC GGT	810
Ala Lys Ile Val Asn Val Cys Asn Trp Ile Leu Ser Ser Ala Ile Gly	
185 190 195	
CTG CCT GTA ATG TTC ATG GCA ACC ACA AAA TAC AGG CAG GGG TCC ATA	858
Leu Pro Val Met Phe Met Ala Thr Thr Lys Tyr Arg Gln Gly Ser Ile	
200 205 210 215	
GAT TGC ACC CTC ACG TTC TCC CAC CCA ACC TGG TAC TGG GAG AAC CTG	906
Asp Cys Thr Leu Thr Phe Ser His Pro Thr Trp Tyr Trp Glu Asn Leu	
220 225 230	
CTC AAA ATC TGT GTC TTT ATC TTC GCT TTC ATC ATG CCG ATC CTC ATC	954
Leu Lys Ile Cys Val Phe Ile Phe Ala Phe Ile Met Pro Ile Leu Ile	
235 240 245	
ATC ACT GTG TGT TAC GGC CTG ATG ATC TTA CGA CTC AAG AGC GTT CGC	1002
Ile Thr Val Cys Tyr Gly Leu Met Ile Leu Arg Leu Lys Ser Val Arg	
250 255 260	
ATG CTA TCG GGC TCC AAA GAA AAG GAC AGG AAT CTG CGC AGG ATC ACC	1050
Met Leu Ser Gly Ser Lys Glu Lys Asp Arg Asn Leu Arg Arg Ile Thr	
265 270 275	

CGG	ATG	GTG	CTG	GTG	GTC	GTG	GCT	GTA	TTT	ATC	GTC	TGC	TGG	ACC	CCC	1098
Arg	Met	Val	Leu	Val	Val	Val	Ala	Val	Phe	Ile	Val	Cys	Trp	Thr	Pro	
280					285					290					295	
ATC	CAC	ATC	TAC	GTC	ATC	ATC	AAA	GCG	CTG	ATC	ACG	ATT	CCA	GAA	ACC	1146
Ile	His	Ile	Tyr	Val	Ile	Ile	Lys	Ala	Leu	Ile	Thr	Ile	Pro	Glu	Thr	
				300					305					310		
ACA	TTT	CAG	ACC	GTT	TCC	TGG	CAC	TTC	TGC	ATT	GCT	TTG	GGT	TAC	ACG	1194
Thr	Phe	Gln	Thr	Val	Ser	Trp	His	Phe	Cys	Ile	Ala	Leu	Gly	Tyr	Thr	
			315					320					325			
AAC	AGC	TGC	CTG	AAT	CCA	GTT	CTT	TAC	GCC	TTC	CTG	GAT	GAA	AAC	TTC	1242
Asn	Ser	Cys	Leu	Asn	Pro	Val	Leu	Tyr	Ala	Phe	Leu	Asp	Glu	Asn	Phe	
		330					335					340				
AAG	CGA	TGC	TTC	AGA	GAG	TTC	TGC	ATC	CCA	ACC	TCG	TCC	ACG	ATC	GAA	1290
Lys	Arg	Cys	Phe	Arg	Glu	Phe	Cys	Ile	Pro	Thr	Ser	Ser	Thr	Ile	Glu	
	345				350						355					
CAG	CAA	AAC	TCC	ACT	CGA	GTC	CGT	CAG	AAC	ACT	AGG	GAA	CAT	CCC	TCC	1338
Gln	Gln	Asn	Ser	Thr	Arg	Val	Arg	Gln	Asn	Thr	Arg	Glu	His	Pro	Ser	
360					365					370				375		
ACG	GCT	AAT	ACA	GTG	GAT	CGA	ACT	AAC	CAC	CAG	CTA	GAA	AAT	CTG	GAG	1386
Thr	Ala	Asn	Thr	Val	Asp	Arg	Thr	Asn	His	Gln	Leu	Glu	Asn	Leu	Glu	
				380				385						390		
GCA	GAA	ACT	GCT	CCA	TTG	CCC	TAAGTGGGTC	TCACACCATC	CAGACCCTCG							1437
Ala	Glu	Thr	Ala	Pro	Leu	Pro										
			395													
CTAAGCTTAG	AGGCCGCCAT	CTACGCGGAA	TCAGGTTGCT	GTCAGGGTGT	GTGGGAGGCT											1497
CTGGTTTCCT	GAGAAACCAT	CTGATCCTGC	ATTCAAAGTC	ATTCCTCTCT	GGCTACTTCA											1557
CTCTGCACAT	GAGAGATGCT	CAGACTGATC	AAGACCAGAA	GAAAGAAGAG	ACTACCGGAC											1617
A																1618

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Asp	Ser	Ser	Thr	Gly	Pro	Gly	Asn	Thr	Ser	Asp	Cys	Ser	Asp	Pro
1				5					10					15	
Leu	Ala	Gln	Ala	Ser	Cys	Ser	Pro	Ala	Pro	Gly	Ser	Trp	Leu	Asn	Leu
			20					25					30		
Ser	His	Val	Asp	Gly	Asn	Gln	Ser	Asp	Pro	Cys	Gly	Leu	Asn	Arg	Thr
		35				40					45				
Gly	Leu	Gly	Gly	Asn	Asp	Ser	Leu	Cys	Pro	Gln	Thr	Gly	Ser	Pro	Ser
	50				55					60					
Met	Val	Thr	Ala	Ile	Thr	Ile	Met	Ala	Leu	Tyr	Ser	Ile	Val	Cys	Val
65					70					75				80	

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Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val Arg Tyr
85 90 95

Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu Ala Leu
100 105 110

Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val Asn Tyr
115 120 125

Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile Val Ile
130 135 140

Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu Cys Thr
145 150 155 160

Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys Ala Leu
165 170 175

Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Val Asn Val Cys Asn Trp
180 185 190

Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala Thr Thr
195 200 205

Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser His Pro
210 215 220

Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile Phe Ala
225 230 235 240

Phe Ile Met Pro Ile Leu Ile Ile Thr Val Cys Tyr Gly Leu Met Ile
245 250 255

Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu Lys Asp
260 265 270

Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val Ala Val
275 280 285

Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile Lys Ala
290 295 300

Leu Ile Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp His Phe
305 310 315 320

Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val Leu Tyr
325 330 335

Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe Cys Ile
340 345 350

Pro Thr Ser Ser Thr Ile Glu Gln Gln Asn Ser Thr Arg Val Arg Gln
355 360 365

Asn Thr Arg Glu His Pro Ser Thr Ala Asn Thr Val Asp Arg Thr Asn
370 375 380

His Gln Leu Glu Asn Leu Glu Ala Glu Thr Ala Pro Leu Pro
385 390 395

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (cDNA)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 339..1235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGTGGAAGGG GGCTACAAGC AGAGGAGAAT ATCAGACGCT CAGACGTTCC CTTCTGCCTG 60
CCGCTCTTCT CTGGTTCCAC TAGGGCTGGT CCATGTAAGA ATCTGACGGA GCCTAGGGCA 120
GCTGTGAGAG GAAGAGGCTG GGGCGCGTGG AACCCGAAAA GTCTGAGTGC TCTCAGTTAC 180
AGCCTACCTA GTCCGCAGCA GGCCTTCAGC ACCATGGACA GCAGCACCGG CCCAGGGAAC 240
ACCAGCGACT GCTCAGACCC CTTAGCTCAG GCAAGTTGCT CCCCAGCACC TGGCTCCTGG 300
CTCAACTTGT CCCACGTTGA TGGCAACCAG TCCGATCC ATG CGG TCT GAA CCG 353
Met Arg Ser Glu Pro
1 5
CAC CGG GCT TGG CGG GAA CGA CAG CCT GTG CCC TCA GAC CGG CAG CCC 401
His Arg Ala Trp Arg Glu Arg Gln Pro Val Pro Ser Asp Arg Gln Pro
10 15 20
TTC CAT GGT CAC AGC CAT TAC CAT CAT GGC CCT CTA CTC TAT CGT GTG 449
Phe His Gly His Ser His Tyr His His Gly Pro Leu Leu Tyr Arg Val
25 30 35
TGT AGT GGG CCT CTT CGG AAA CTT CCT GGT CAT GTA TGT GAT TGT AAG 497
Cys Ser Gly Pro Leu Arg Lys Leu Pro Gly His Val Cys Asp Cys Lys
40 45 50
ATA CAC CAA AAT GAA GAC TGC CAC CAA CAT CTA CAT TTT CAA CCT TGC 545
Ile His Gln Asn Glu Asp Cys His Gln His Leu His Phe Gln Pro Cys
55 60 65
TCT GGC AGA CGC CTT AGC GAC CAG TAC ACT GCC CTT TCA GAG TGT CAA 593
Ser Gly Arg Arg Leu Ser Asp Gln Tyr Thr Ala Leu Ser Glu Cys Gln
70 75 80 85
CTA CCT GAT GGG AAC ATG GCC CTT GGG AAC CAT CCT CTG CAA GAT CGT 641
Leu Pro Asp Gly Asn Met Ala Leu Arg Asn His Pro Leu Gln Asp Arg
90 95 100
GAT CTC AAT AGA TTA CTA CAA CAT GTT CAC CAG CAT ATT CAC CCT CTG 689
Asp Leu Asn Arg Leu Leu Gln His Val His Gln His Ile His Pro Leu
105 110 115
CAC CAT GAG CGT GGA CCG CTA CAT TGC TGT CTG CCA CCC AGT CAA AGC 737
His His Glu Arg Gly Pro Leu His Cys Cys Leu Pro Pro Ser Gln Ser
120 125 130
CCT GGA TTT CCG TAC CCC CCG AAA TGC CAA AAT CGT CAA CGT CTG CAA 785
Pro Gly Phe Pro Tyr Pro Pro Lys Cys Gln Asn Arg Gln Arg Leu Gln
135 140 145

CTG GAT CCT CTC TTC TGC CAT CGG TCT GCC TGT AAT GTT CAT GGC AAC	833
Leu Asp Pro Leu Phe Cys His Arg Ser Ala Cys Asn Val His Gly Asn	
150 155 160 165	
CAC AAA ATA CAG GCA GGG GTC CAT AGA TTG CAC CCT CAC GTT CTC CCA	881
His Lys Ile Gln Ala Gly Val His Arg Leu His Pro His Val Leu Pro	
170 175 180	
CCC AAC CTG GTA CTG GGA GAA CCT GCT CAA AAT CTG TGT CTT TAT CTT	929
Pro Asn Leu Val Leu Gly Glu Pro Ala Gln Asn Leu Cys Leu Tyr Leu	
185 190 195	
CGC TTT CAT CAT GCC GAT CCT CAT CAT CAC TGT GTG TTA CGG CCT GAT	977
Arg Phe His His Ala Asp Pro His His His Cys Val Leu Arg Pro Asp	
200 205 210	
GAT CTT ACG ACT CAA GAG CGT TCG CAT GCT ATC GGG CTC CAA AGA AAA	1025
Asp Leu Thr Thr Gln Glu Arg Ser His Ala Ile Gly Leu Gln Arg Lys	
215 220 225	
GGA CAG GAA TCT GCG CAG GAT CAC CCG GAT GGT GCT GGT GGT CGT GGC	1073
Gly Gln Glu Ser Ala Gln Asp His Pro Asp Gly Ala Gly Gly Arg Gly	
230 235 240 245	
TGT ATT TAT CGT CTG CTG GAC CCC CAT CCA CAT CTA CGT CAT CAT CAA	1121
Cys Ile Tyr Arg Leu Leu Asp Pro His Pro His Leu Arg His His Gln	
250 255 260	
AGC GCT GAT CAC GAT TCC AGA AAC CAC ATT TCA GAC CGT TTC CTG GCA	1169
Ser Ala Asp His Asp Ser Arg Asn His Ile Ser Asp Arg Phe Leu Ala	
265 270 275	
CTT CTG CAT TGC TTT GGG TTA CAC GAA CAG CTG CCT GAA TCC AGT TCT	1217
Leu Leu His Cys Phe Gly Leu His Glu Gln Leu Pro Glu Ser Ser Ser	
280 285 290	
TTA CGC CTT CCT GGA TGAAACTTC AAGCGATGCT TCAGAGAGTT CTGCATCCCA	1272
Leu Arg Leu Pro Gly	
295	
ACCTCGTCCA CGATCGAACA GCAAACTCC ACTCGAGTCC GTCAGAACAC TAGGGAACAT	1332
CCCTCCACGG CTAATACAGT GGATCGAACT AACCACCAGC TAGAAAATCT GGAGGCAGAA	1392
ACTGCTCCAT TGCCCTAACT GGGTCTCACA CCATCCAGAC CCTCGCTAAG CTTAGAGGCC	1452
GCCATCTACG TGGAATCAGG TTGCTGTCAG GGTGTGTGGG AGGCTCTGGT TTCCTGAGAA	1512
ACCATCTGAT CCTGCATTCA AAGTCATTCC TCTCTGGCTA CTTCACTCTG CACATGAGAG	1572
ATGCTCAGAC TGATCAAGAC CAGAAGAAAG AAGAGACTAC CGGACA	1618

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Arg	Ser	Glu	Pro	His	Arg	Ala	Trp	Arg	Glu	Arg	Gln	Pro	Val	Pro
1				5					10					15	

*Sub
B1
cont*

Ser Asp Arg Gln Pro Phe His Gly His Ser His Tyr His His Gly Pro
20 25 30

Leu Leu Tyr Arg Val Cys Ser Gly Pro Leu Arg Lys Leu Pro Gly His
35 40 45

Val Cys Asp Cys Lys Ile His Gln Asn Glu Asp Cys His Gln His Leu
50 55 60

His Phe Gln Pro Cys Ser Gly Arg Arg Leu Ser Asp Gln Tyr Thr Ala
65 70 75 80

Leu Ser Glu Cys Gln Leu Pro Asp Gly Asn Met Ala Leu Arg Asn His
85 90 95

Pro Leu Gln Asp Arg Asp Leu Asn Arg Leu Leu Gln His Val His Gln
100 105 110

His Ile His Pro Leu His His Glu Arg Gly Pro Leu His Cys Cys Leu
115 120 125

Pro Pro Ser Gln Ser Pro Gly Phe Pro Tyr Pro Pro Lys Cys Gln Asn
130 135 140

Arg Gln Arg Leu Gln Leu Asp Pro Leu Phe Cys His Arg Ser Ala Cys
145 150 155 160

Asn Val His Gly Asn His Lys Ile Gln Ala Gly Val His Arg Leu His
165 170 175

Pro His Val Leu Pro Pro Asn Leu Val Leu Gly Glu Pro Ala Gln Asn
180 185 190

Leu Cys Leu Tyr Leu Arg Phe His His Ala Asp Pro His His His Cys
195 200 205

Val Leu Arg Pro Asp Asp Leu Thr Thr Gln Glu Arg Ser His Ala Ile
210 215 220

Gly Leu Gln Arg Lys Gly Gln Glu Ser Ala Gln Asp His Pro Asp Gly
225 230 235 240

Ala Gly Gly Arg Gly Cys Ile Tyr Arg Leu Leu Asp Pro His Pro His
245 250 255

Leu Arg His His Gln Ser Ala Asp His Asp Ser Arg Asn His Ile Ser
260 265 270

Asp Arg Phe Leu Ala Leu Leu His Cys Phe Gly Leu His Glu Gln Leu
275 280 285

Pro Glu Ser Ser Ser Leu Arg Leu Pro Gly
290 295

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (cDNA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATCTTCACCC TCACCATGAT G

21

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (cDNA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGGTCCTTCT CCTTGAACC

20

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